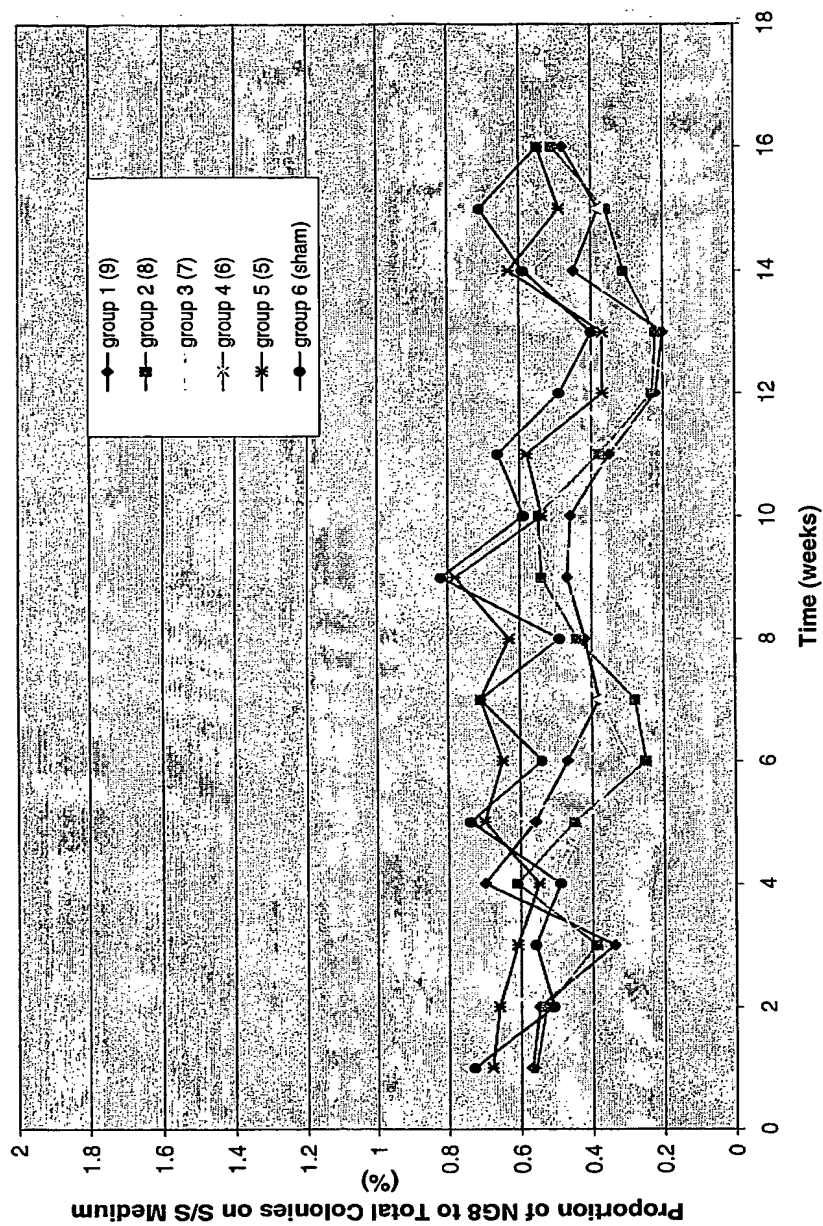Caries Probiotic Study

FIGURE 2A

Comparison of *S. mutans* JH145 LDH gene to *S. mutans* BHT-2 LDH gene.

ldh Start: base 486 (Bold)
JH145 mutation: 1 bp deletion at base 718 of BHT-2
ldh Stop: base 1474/BHT-2 and 1473/JH145 (Underline)

JH145: 191 tcacgaacatctggcagggcacgagaaacaataacactcatagcatagtcaataaaactc 250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 191 tcacgaacatctggcagggcacgagaaacaataacactcatagcatagtcaataaaactc 250

JH145: 251 gttttcatttcactcgttaaattaacatctactaaatttctatcttgcattaaaaaatgc 310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 251 gttttcatttcactcgttaaattaacatctactaaatttctatcttgcattaaaaaatgc 310

JH145: 311 tccatttctagtctaaaactcctttatattatatcacaaaaaatgctcttttcagctat 370
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 311 tccatttctagtctaaaactcctttatattatatcacaaaaaatgctcttttcagctat 370

JH145: 371 tctactatagttttcctttaacagaggaaaatactagtgactttttaacaaaaagtgtt 430
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 371 tctactatagttttcctttaacagaggaaaatactagtgactttttaacaaaaagtgtt 430

JH145: 431 agaataaattcgtataaaatatacacttaataaattataaggagatgtttagaacatgac 490
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 431 agaataaattcgtataaaatatacacttaataaattataaggagatgtttagaacatgac 490

JH145: 491 tgcaactaaacaacataaaaaagtcatccttgtcggtgatggtgctgtaggatcatctta 550
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 491 tgcaactaaacaacataaaaaagtcatccttgtcggtgatggtgctgtaggatcatctta 550

JH145: 551 cgccttcgcccttgttaaccaaggaatcgctcaagaactcggaattattgaaattcctca 610
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 551 cgccttcgcccttgttaaccaaggaatcgctcaagaactcggaattattgaaattcctca 610

JH145: 611 gctgtttgaaaaggctgttggagacgctcttgaccttagccatgcacttgccttcacttc 670
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 611 gctgtttgaaaaggctgttggagacgctcttgaccttagccatgcacttgccttcacttc 670

JH145: 671 accaaagaaaatttacgctgctaaatatgaagactgtgcggatgctg-ccttgttgtcat 729
            ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
BHT-2: 671 accaaagaaaatttacgctgctaaatatgaagactgtgcggatgctgaccttgttgtcat 730

JH145: 730 tactgcaggtgcacctcaaaaaccaggtgaaactcgtcttgaccttgtcggtaaaaacct 789
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2: 731 tactgcaggtgcacctcaaaaaccaggtgaaactcgtcttgaccttgtcggtaaaacct 790

FIGURE 2B

```
JH145:  790  tgcaatcaacaaatctatcgttacacaagtggttgaatcaggcctttaagggaatcttctt  849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  791  tgcaatcaacaaatctatcgttacacaagtggttgaatcaggcctttaagggaatcttctt  850


JH145:  850  ggttgctgccaacccagttgacatcttgacttattcaacatggaaattctcaggtttccc  909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  851  ggttgctgccaacccagttgacatcttgacttattcaacatggaaattctcaggtttccc  910


JH145:  910  taaagaacgcgtcattggttctggtacatctcttgatactgctcgtttccgtcaagctct  969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  911  taaagaacgcgtcattggttctggtacatctcttgatactgctcgtttccgtcaagctct  970


JH145:  970  tgctgaaaaaatcggggttgatgctcggtcagtccacgcctatatcatgggtgaacacgg  1029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  971  tgctgaaaaaatcggggttgatgctcggtcagtccacgcctatatcatgggtgaacacgg  1030


JH145:  1030 tgattcagaatttgccgtttggtctcatgccaatgtagctggtgttaaattagaacaatg  1089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1031 tgattcagaatttgccgtttggtctcatgccaatgtagctggtgttaaattagaacaatg  1090


JH145:  1090 gctgcaagacaaccgtgatgttgatgctgaaggtctcgtaaaactgtttgtatctgttcg  1149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1091 gctgcaagacaaccgtgatgttgatgctgaaggtctcgtaaaactgtttgtatctgttcg  1150


JH145:  1150 tgatgctgcttattcaatcatcaacaaaaaaggtgctactttctatggtatcgctgtcgc  1209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1151 tgatgctgcttattcaatcatcaacaaaaaaggtgctactttctatggtatcgctgtcgc  1210


JH145:  1210 ccttgcccgtatcactaaagcaatcttggatgacgaaaacgccgttcttccgctttcagt  1269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1211 ccttgcccgtatcactaaagcaatcttggatgacgaaaacgccgttcttccgctttcagt  1270


JH145:  1270 tttccaatcaggccaatacgaaggtgttgaagatgtcttcatcggacagccggccatcgt  1329
             |||||||.||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1271 tttccaatcaggccaatacgaaggtgttgaagatgtcttcatcggacagccggccatcgt  1330


JH145:  1330 tggtgcacacggtatcgttcgtccagtaaatattccgttaaatgatgctgaactgcaaaa  1389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1331 tggtgcacacggtatcgttcgtccagtaaatattccgttaaatgatgctgaactgcaaaa  1390


JH145:  1390 aatgcaggcttctgctaaacagctgaaagcaatcattgacgaagctttctcaaatgaaga  1449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
BHT-2:  1391 aatgcaggcttctgctaaacagctgaaagcaatcattgacgaagctttctcaaatgaaga  1450


JH145:  1450 atttgctgctgctgcagctcgtaa  1473 SEQ ID NO:1
             ||||||||||||||||||||||||
BHT-2:  1451 atttgctgctgctgcagctcgtaa  1474 SEQ ID NO:9
```

FIGURE 2C

BHT-2 Protein Sequence where (—) indicates a stop codon (SEQ ID NO:10).

```
1    MTATKQHKKVILVGDGAVGSSYAFALVNQGIAQELGIIEIPQLFEKAVGD  50
51   ALDLSHALAFTSPKKIYAAKYEDCADADLVVITAGAPQKPGETRLDLVGK  100
101  NLAINKSIVTQVVESGFKGIFLVAANPVDILTYSTWKFSGFPKERVIGSG  150
151  TSLDTARFRQALAEKIGVDARSVHAYIMGEHGDSEFAVWSHANVAGVKLE  200
201  QWLQDNRDVDAEGLVKLFVSVRDAAYSIINKKGATFYGIAVALARITKAI  250
251  LDDENAVLPLSVFQSGQYEGVEDVFIGQPAIVGAHGIVRPVNIPLNDAEL  300
301  QKMQASAKQLKAIIDEAFSNEEFAAAAAR—                      329
```

JH145 Protein Sequence where (—) indicates a stop codon (SEQ ID NOs:2-8).

```
1    MTATKQHKKVILVGDGAVGSSYAFALVNQGIAQELGIIEIPQLFEKAVGD  50
51   ALDLSHALAFTSPKKIYAAKYEDCADAALLSLLQVHLKNQVKLVLTLSVK  100
101  TLQSTNLSLHKWLNQALRESSWLLPTQLTS—LIQHGNSQVSLKNASLVLV  150
151  HLLILLVSVKLLLKKSGLMLGQSTPISWVNTVIQNLPFGLMPM—LVLN—N  200
201  NGCKTTVMLMLKVS—NCLYLFVMLLIQSSTKKVLLSMVSLSPLPVSLKQS  250
251  WMTKTPFFRFQFSNQANTKVLKMSSSDSRPSLVHTVSFVQ—IFR—MMLNC  300
301  KKCRLLLNS—KQSLTKLSQMKNLLLLQLV                        329
```